17P4

The *Rhodobacter sphaeroides* F_0F_1-ATPase activity: Effects of heavy metal ions and relationship with hydrogen photoproduction

L. Gabrielyan[1], L. Hakobyan[1], A. Trchounian[1,2]
[1]*Yerevan State University, Department of Biophysics, Yerevan 0025, Armenia*
[2]*Yerevan State University, Department of Microbiology & Plant and Microbe Biotechnology, Yerevan 0025, Armenia*
E-mail: lgabrielyan@ysu.am

The important aspect in regulation of hydrogen (H_2) photoproduction by purple bacteria and its energetics is the requirement of the F_0F_1-ATPase, the main membrane mechanism generating proton motive force [1,2]. Previously the relationship between H_2 production, proton transport and the F_0F_1-ATPase activity was shown by purple bacteria *Rhodobacter sphaeroides* [2]. It is well known that H_2 production varies depending on the different factors: anaerobic conditions, light intensity, pH, carbon and nitrogen sources, and heavy metals ions [3,4]. Fe, Ni and Mo ions are the components of enzymes, which are responsible for H_2 production by photosynthetic bacteria, such as hydrogenase and nitrogenase. Bacterial photosynthetic pigments such as bacteriochlorophyll contain Mg.

R. sphaeroides MDC 6521 (isolated from Arzni mineral springs in Armenia) is able to grow and produce H_2 in anaerobic conditions under illumination in the presence of various heavy metal ions [4]. In this study in order to examine the mediatory role of the F_0F_1-ATPase in H_2 production, the effects of metal ions (Ni^{2+}, Mg^{2+}, Mo^{6+}, and Fe^{2+}) on DCCD inhibited ATPase activity of *R. sphaeroides* membrane vesicles were investigated.

These metal ions in appropriate concentrations considerably enhanced H_2 production by *R. sphaeroides*. But H_2 production was not observed in the absence of Fe^{2+}, indicating that Fe^{2+} is required for H_2 production. As was shown in our previous study [2] the *R. sphaeroides* membrane vesicles demonstrated significant ATPase activity. The absence of Fe^{2+} caused to marked inhibition (~80%) in ATPase activity. After treatment of membrane vesicles with Ni^{2+} (0.004 mM) and Mg^{2+} (10 mM) the ATPase activity stimulation was observed: the activity was increased by 15 and 30%, respectively. The Fe^{2+} (0.08 mM) and Mo^{6+} (0.016 mM) added gave a stimulated (~2.5 fold) ATPase activity.

These results indicate a relationship between the F_0F_1-ATPase activity and H_2 photoproduction. This provides novel evidence on the role of the F_0F_1-ATPase in H_2 production by this bacterium.

References

[1] L. Hakobyan, L. Gabrielyan, A. Trchounian, Curr. Microbiol. 62 (2011) 415–419.
[2] L. Gabrielyan, A. Trchounian, Int. J. Hydrogen Energy 34 (2009) 2567–2572.
[3] L. Gabrielyan, H. Torgomyan, A. Trchounian, Int. J. Hydrogen Energy 35 (2010) 12201–12207.
[4] L. Hakobyan, L. Gabrielyan, A. Trchounian, Int. J. Hydrogen Energy 37 (2012) 7482–7486.

doi:10.1016/j.bbabio.2012.06.352

17P5

Regulation of anaerobic glycolysis during work transitions in skeletal muscle: In silico studies

B. Korzeniewski, J.A. Zoladz
Jagiellonian University, Faculty of Biochemistry, Biophysics and Biotechnology, Gronostajowa 7, PL-30-387 Krakow, Poland
AWF Krakow, Department of Physiology and Biochemistry, Jana Pawla II 78, PL-31-571, Krakow, Poland
E-mail: bernard.korzeniewski@uj.edu.pl

The regulation of anaerobic glycolysis in response to elevated ATP demand at the onset of exercise in skeletal muscle is still not fully understood [1]. The computer model of the bioenergetic system in skeletal muscle, comprising oxidative phosphorylation, creatine kinase, anaerobic glycolysis and ATP usage developed previously [2] was used to study the regulation and impact on the system of anaerobic glycolysis during on- (rest-to-work) and off- (work-to-rest) transients. It is shown that changes in ADP_{free} and related metabolites cannot account for the huge increase in the glycolytic flux during on-transient. It is demonstrated that, while the postulated direct activation of glycolysis and glycogenolysis is able to elevate the glycolytic flux and decrease pH during muscle contraction significantly, great changes in oxygen concentration in the physiological range exert much smaller effect on the glycolytic flux and pH. Computer simulations reveal that anaerobic glycolysis slows down the VO_2 and PCr on-kinetics. It is also shown that anaerobic glycolysis removes the PCr recovery overshoot. Computer simulations predict, in accordance with experimental data [3], that PCr cannot be rebuilt after exercise in anoxia, although the concentration of ADP_{free}, an activator of glycolysis, is significantly increased. Finally, it is demonstrated that the relationship between the initial phase of the VO_2 off-kinetics and the PCr off-kinetics is inverse: the faster the initial phase of the VO_2 off-kinetics, the slower the PCr off-kinetics, and inversely. However, a faster initial phase of the VO_2 off-kinetics is associated with a slower late phase of this kinetics; as a result the integral of VO_2 (above the baseline) representing the total oxygen debt is identical in different cases for the same decrease of PCr during work.

References

[1] R.J. Connet, K. Sahlin, Control of glycolysis and glycogen metabolism, In: in: L.B. Rowell, J.T. Shepherd (Eds.), Handbook of Physiology, Oxford University Press, New York, 1996, pp. 870–911.
[2] B. Korzeniewski, P. Liguzinski, Theoretical studies on the regulation of anaerobic glycolysis and its influence on oxidative phosphorylation in skeletal muscle, Biophys. Chem. 110 (2004) 147–169.
[3] B. Quistorff, L. Johansen, K. Sahlin, Absence of phosphocreatine resynthesis in human calf muscle during ischaemic recovery, Biochem. J. 291 (1992) 681–686.

doi:10.1016/j.bbabio.2012.06.353

17P6

An analysis of amino acid residues which affect the structure of the ion flux pathway of the flagellar stator complex from *Bacillus subtilis*

Kotomi Koyama, Masahiro Ito
Graduate School of Life Sciences and Bio-Nano Electronics Research Centre, Toyo University, Japan
E-mail: gx1100053@toyo.jp

Many bacteria swim by rotating flagellar that consists of a basal body (rotary motor), a helical filament (propeller), and a hook (universal joint). The energy for rotation of the flagellar motor comes from the H^+ or Na^+ gradient across the cytoplasmic membrane. The motor consists of a rotor and some stators, that work as an ion channel. The stators are most often called a Mot complex, that is thought to contain four MotA subunits and two MotB subunits. *Escherichia coli*